

H. Schnitzer

Re-run

1653

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/601,168A

DATE: 06/27/2002

TIME: 13:57:15

Input Set : N:\paola\US09601168A.RAW

Output Set: N:\CRF3\06272002\I601168A.raw

C--> 1 <110> APPLICANT: BENAROUS, Richard
 2 MARGOTTIN, Florence
 3 DURAND, Herve
 4 ARENZANA SEISDEDOS, Fernando
 5 KROLL, Mathias
 6 CONDORCET, Jean-Paul
 7 <120> TITLE OF INVENTION: Human beta-TrCP protein
 8 <130> FILE REFERENCE: 935.38812X00
 9 <140> CURRENT APPLICATION NUMBER: US/09/601,168A
 10 <141> CURRENT FILING DATE: 2000-07-28
 11 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00196
 12 <151> PRIOR FILING DATE: 1999-01-29
 13 <150> PRIOR APPLICATION NUMBER: FR98 01100
 14 <151> PRIOR FILING DATE: 1998-01-30
 15 <150> PRIOR APPLICATION NUMBER: FR98 15545
 16 <151> PRIOR FILING DATE: 1998-12-09
 17 <160> NUMBER OF SEQ ID NOS: 8
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2151
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Artificial sequence
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (70)..(1776)
 27 <223> OTHER INFORMATION: Description of the artificial sequence : cDNA
 28 coding for human beta-TrCP protein
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 31 tcggcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag 111
 32 Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys
 33 1 5 10
 34 ttt atg aat tcc tca gag aga gaa gac tgt aat aat ggc gaa ccc cct 159
 35 Phe Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro
 36 15 20 25 30
 37 agg aag ata ata cca gag aag aat tca ctt aga cag aca tac aac agc 207
 38 Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser
 39 35 40 45
 40 tgt gcc aga ctc tgc tta aac caa gaa aca gta tgt tta gca agc act 255
 41 Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr
 42 50 55 60
 43 gct atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc 303
 44 Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly

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45	act	tcc	agt	atg	att	gtg	ccc	aag	caa	cgg	aaa	ctc	tca	gca	agc	tat	1		
46	Thr	Ser	Ser	Met	Ile	Val	Pro	Lys	Gln	Arg	Lys	Leu	Ser	Ala	Ser	Tyr	2		
47		80										90					3		
48	gaa	aag	gaa	aag	gaa	ctg	tgt	gtc	aaa	tac	ttt	gag	cag	tgg	tca	gag	4		
49	Glu	Lys	Glu	Lys	Glu	Leu	Cys	Val	Lys	Tyr	Phe	Glu	Gln	Trp	Ser	Glu	5		
50		95				100					105					110	6		
51	tca	gat	caa	gtg	gaa	ttt	gtg	gaa	cat	ctt	ata	tcc	caa	atg	tgt	cat	7		
52	Ser	Asp	Gln	Val	Glu	Phe	Val	Glu	His	Leu	Ile	Ser	Gln	Met	Cys	His	8		
53					115					120					125		9		
54	tac	caa	cat	ggg	cac	ata	aac	tcg	tat	ctt	aaa	cct	atg	ttg	cag	aga	10		
55	Tyr	Gln	His	Gly	His	Ile	Asn	Ser	Tyr	Leu	Lys	Pro	Met	Leu	Gln	Arg	11		
56				130					135					140			12		
57	gat	ttc	ata	act	gct	ctg	cca	gct	cgg	gga	ttg	gat	cat	atc	gct	gag	13		
58	Asp	Phe	Ile	Thr	Ala	Leu	Pro	Ala	Arg	Gly	Leu	Asp	His	Ile	Ala	Glu	14		
59			145					150					155				15		
60	aac	att	ctg	tca	tac	ctg	gat	gcc	aaa	tca	cta	tgt	gct	gct	gaa	ctt	16		
61	Asn	Ile	Leu	Ser	Tyr	Leu	Asp	Ala	Lys	Ser	Leu	Cys	Ala	Ala	Glu	Leu	17		
62			160				165					170					18		
63	gtg	tgc	aag	gaa	tgg	tac	cga	gtg	acc	tct	gat	ggc	atg	ctg	tgg	aag	19		
64	Val	Cys	Lys	Glu	Trp	Tyr	Arg	Val	Thr	Ser	Asp	Gly	Met	Leu	Trp	Lys	20		
65		175				180					185				190		21		
66	aag	ctt	atc	gag	aga	atg	gtc	agg	aca	gat	tct	ctg	tgg	aga	ggc	ctg	22		
67	Lys	Leu	Ile	Glu	Arg	Met	Val	Arg	Thr	Asp	Ser	Leu	Trp	Arg	Gly	Leu	23		
68				195						200					205		24		
69	gca	gaa	cga	aga	gga	tgg	gga	cag	tat	tta	ttc	aaa	aac	aaa	cct	cct	25		
70	Ala	Glu	Arg	Arg	Gly	Trp	Gly	Gln	Tyr	Leu	Phe	Lys	Asn	Lys	Pro	Pro	26		
71				210					215					220			27		
72	gac	ggg	aat	gct	cct	ccc	aac	tct	ttt	tat	aga	gca	ctt	tat	cct	aaa	28		
73	Asp	Gly	Asn	Ala	Pro	Pro	Asn	Ser	Phe	Tyr	Arg	Ala	Leu	Tyr	Pro	Lys	29		
74			225					230					235				30		
75	att	ata	caa	gac	att	gag	aca	ata	gaa	tct	aat	tgg	aga	tgt	gga	aga	31		
76	Ile	Ile	Gln	Asp	Ile	Glu	Thr	Ile	Glu	Ser	Asn	Trp	Arg	Cys	Gly	Arg	32		
77			240				245					250					33		
78	cat	agt	tta	cag	aga	att	cac	tgc	cga	agt	gaa	aca	agc	aaa	gga	gtt	34		
79	His	Ser	Leu	Gln	Arg	Ile	His	Cys	Arg	Ser	Glu	Thr	Ser	Lys	Gly	Val	35		
80		255				260					265				270				

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94  aat aca ggt gaa atg cta aac acg ttg att cac cat tgt gaa gca gtt 1119
95  Asn Thr Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val
96  335                               340                               345                               350
97  ctg cac ttg cgt ttc aat aat ggc atg atg gtg acc tgc tcc aaa gat 1167
98  Leu His Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp
99  355                               360                               365
100  cgt tcc att gct gta tgg gat atg gcc tcc cca act gac att acc ctc 1215
101  Arg Ser Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu
102  370                               375                               380
103  cgg agg gtg ctg gtc gga cac cga gct gct gtc aat gtt gta gac ttt 1263
104  Arg Arg Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe
105  385                               390                               395
106  gat gac aag tac att gtt tct gca tct ggg gat aga act ata aag gta 1311
107  Asp Asp Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val
108  400                               405                               410
109  tgg aac aca agt act tgt gaa ttt gta agg acc tta aat gga cac aaa 1359
110  Trp Asn Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys
111  415                               420                               425                               430
112  cga ggc att gcc tgt ttg cag tac agg gac agg ctg gta gtg agt ggc 1407
113  Arg Gly Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly
114  435                               440                               445
115  tca tct gac aac act atc aga tta tgg gac ata gaa tgt ggt gca tgt 1455
116  Ser Ser Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys
117  450                               455                               460
118  tta cga gtg tta gaa ggc cat gag gaa ttg gtg cgt tgt att cga ttt 1503
119  Leu Arg Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe
120  465                               470                               475
121  gat aac aag agg ata gtc agt ggg gcc tat gat gga aaa att aaa gtg 1551
122  Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val
123  480                               485                               490
124  tgg gat ctt gtg gct gct ttg gac ccc cgt gct cct gca ggg aca ctc 1599
125  Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu
126  495                               500                               505                               510
127  tgt cta cgg acc ctt gtg gag cat tcc gga aga gtt ttt cga cta cag 1647
128  Cys Leu Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln
129  515                               520                               525
130  ttt gat gaa ttc cag att gtc agt agt tca cat gat gac aca atc ctc 1695
131  Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu
132  530                               535                               540
133  atc tgg gac ttc cta aat gat cca gct gcc caa gct gaa ccc ccc cgt 1743
134  Ile Trp Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg
135  545                               550                               555
136  tcc cct tct cga aca tac acc tac atc tcc aga taaataacca tacactgacc 1796
137  Ser Pro Ser Arg Thr Tyr Thr Tyr Ile Ser Arg
138  560                               565
139  tcatacttgc ccaggaccca ttaaagtgtc ggtatttaac gtatctgccca ataccaggat 1856
140  gagcaacaac agtaacaatc aaactactgc ccagtttccc tggactagcc gaggagcagg 1916
141  gctttgagac tcctgttggg acacagttgg tctgcagtcg gcccaggacg gtctactcag 1976
142  cacaactgac tgcttcagtg ctgctatcag aagatgtctt ctatcaattg tgaatgattg 2036

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143      gaacttttaa acctcccctc ctctcctcct ttcacctctg cacctagttt tttcccattg 2096
144      gttccagaca aaggtgactt ataaatatat ttagtgtttt gccagaaaaa aaaaa 2151
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147 <211> LENGTH: 569
148 <212> TYPE: PRT
149 <213> ORGANISM: Artificial sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: Description of the artificial sequence : cDNA
152      coding for human beta-TrCP protein
153 <400> SEQUENCE: 2
154      Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met
155           1           5           10           15
156      Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys
157           20           25           30
158      Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala
159           35           40           45
160      Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr Ala Met
161           50           55           60
162      Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly Thr Ser
163           65           70           75           80
164      Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys
165           85           90           95
166      Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp
167           100          105          110
168      Gln Val Glu Phe Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln
169           115          120          125
170      His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe
171           130          135          140
172      Ile Thr Ala Leu Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile
173           145          150          155          160
174      Leu Ser Tyr Leu Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys
175           165          170          175
176      Lys Glu Trp Tyr Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu
177           180          185          190
178      Ile Glu Arg Met Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu
179           195          200          205
180      Arg Arg Gly Trp Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Gly
181           210          215          220
182      Asn Ala Pro Pro Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile
183           225          230          235          240
184      Gln Asp Ile Glu Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser
185           245          250          255
186      Leu Gln Arg Ile His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys
187           260          265          270
188      Leu Gln Tyr Asp Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr
189           275          280          285
190      Ile Lys Ile Trp Asp Lys Asn Thr Leu Glu Cys Lys Arg Ile Leu Thr
191           290          295          300
192      Gly His Thr Gly Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile

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194	Ile Thr Gly Ser Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Thr			
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196	Gly Glu Met Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His			
197		340	345	350
198	Leu Arg Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser			
199		355	360	365
200	Ile Ala Val Trp Asp Met Ala Ser Pro Thr Asp Ile Thr Leu Arg Arg			
201		370	375	380
202	Val Leu Val Gly His Arg Ala Ala Val Asn Val Val Asp Phe Asp Asp			
203		385	390	395
204	Lys Tyr Ile Val Ser Ala Ser Gly Asp Arg Thr Ile Lys Val Trp Asn			
205		405	410	415
206	Thr Ser Thr Cys Glu Phe Val Arg Thr Leu Asn Gly His Lys Arg Gly			
207		420	425	430
208	Ile Ala Cys Leu Gln Tyr Arg Asp Arg Leu Val Val Ser Gly Ser Ser			
209		435	440	445
210	Asp Asn Thr Ile Arg Leu Trp Asp Ile Glu Cys Gly Ala Cys Leu Arg			
211		450	455	460
212	Val Leu Glu Gly His Glu Glu Leu Val Arg Cys Ile Arg Phe Asp Asn			
213		465	470	475
214	Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys Val Trp Asp			
215		485	490	495
216	Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr Leu Cys Leu			
217		500	505	510
218	Arg Thr Leu Val Glu His Ser Gly Arg Val Phe Arg Leu Gln Phe Asp			
219		515	520	525
220	Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile Leu Ile Trp			
221		530	535	540
222	Asp Phe Leu Asn Asp Pro Ala Ala Gln Ala Glu Pro Pro Arg Ser Pro			
223		545	550	555
224	Ser Arg Thr Tyr Thr Tyr Ile Ser Arg			
225		565		
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228	<211> LENGTH: 19			
229	<212> TYPE: DNA			
230	<213> ORGANISM: Artificial sequence			
231	<220> FEATURE:			
232	<223> OTHER INFORMATION: Description of the artificial sequence : sense primer			
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237	<211> LENGTH: 20			
238	<212> TYPE: DNA			
239	<213> ORGANISM: Artificial sequence			
240	<220> FEATURE:			
241	<223> OTHER INFORMATION: Description of the artificial sequence : antisense primer			
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RAW SEQUENCE LISTING ERROR SUMMARY
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The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:4; Line(s) 241

Seq#:6; Line(s) 259

VERIFICATION SUMMARY

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Input Set : N:\paola\US09601168A.RAW

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L:9 M:270 C: Current Application Number differs, Wrong Format